



;ID T24306 standard; cDNA to mRNA; 293 BP.

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;AC

T24306;

;DT 22-SEP-1996 (first entry)

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;DE Human gene signature HUMGS06330.

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;KW Gene signature; messenger RNA; mRNA; relative abundance; frequency;

;KW human; cloning; mapping; non-biased library; diagnosis; detection;

;KW cell typing; abnormal cell function; ss.

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;OS Homo sapiens.

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;PN WO9514772-A1.

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;PD 01-JUN-1995.

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;PF 11-NOV-1994; 94WO-JP01916.

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;PR 12-NOV-1993; 93JP-0355504.

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;PA (MATS/) MATSUBARA K.

;PA (OKUB/) OKUBO K.

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;PI Matsubara K, Okubo K;

;XX

;DR WPI; 1995-206931/27.

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;PT Identifying gene signatures in 3'-directed human cDNA library - e.g.

;PT for diagnosis of abnormal cell function, by preparing cDNA that

;PT reflects relative abundance of corresp. mRNA in specific human

;PT tissues

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;PS Claim 1; Page 1579; 2245pp; Japanese.

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;CC A single-stranded DNA (or its complementary strand or the corresp.
;CC double-stranded DNA) which comprises one of the 7837 "GS" sequences
;CC given in T19001-T26837 and which is able to hybridise to part of
;CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature)
;CC sequences were obtained from 3'-directed cDNA libraries prepared
;CC from various human tissues; synthesis of cDNA was initiated from the
;CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-
;CC untranslated sequence is unique to a particular mRNA species, almost
;CC all the 3'-oriented cDNAs hybridise with specific mRNAs. Each library
;CC is constructed so as to reflect accurately the relative abundance of
;CC different mRNAs in the particular tissue from which it was derived.
;CC The appearance frequency of a given GS in a cDNA library can be
;CC determined (esp. using primers and probes derived from the GS
;CC sequences) as a means of diagnosing abnormal cell function or for
;CC recognising different cell types.

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;SQ Sequence 293 BP; 81 A; 51 C; 51 G; 95 T; 15 other;

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PSN_T24306

gatccagccatnactaacctatnccnnttttggggaaatctgagcctagctcagaaaaacataaagcacc
ttgaaaaagacttggcagcttccngataaagcgtgctgtgctgtgcagtaggancacatcctattttattg
tgatgttgtggttttattatcttaaaactctgntccatacacttgtataaatacatggatatttttatgta
cagaggtagtctctcttaaccagttcacttattgtntctctggcaatttaanganngtcagtaaattnttt
tntctgtnaaagn1

A1 - 09/706,968